

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hillman, Jennifer L.  
Corley, Neil C.  
Baughn, Mariah R.

(ii) TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE  
HOMOLOG

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: HEREWITH  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Cerrone, Michael C  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PP-0532 US

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-855-0572  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: PROSNON01

(B) CLONE: 2278458

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Val Gly Phe Ile Gly Ala Gly Gln Leu Ala Tyr Arg Phe Thr  
 1               5               10               15  
 Ala Ala Gly Ile Leu Ser Ala His Lys Ile Ile Ala Ser Ser Pro Glu  
 20              25              30  
 Met Asn Leu Pro Thr Val Ser Ala Leu Arg Lys Met Gly Val Asn Leu  
 35              40              45  
 Thr Arg Ser Asn Lys Glu Thr Val Lys His Ser Asp Val Leu Phe Leu  
 50              55              60  
 Ala Val Lys Pro His Ile Ile Pro Phe Ile Leu Asp Glu Ile Gly Ala  
 65              70              75              80  
 Asp Val Gln Ala Arg His Ile Val Val Ser Cys Ala Ala Gly Val Thr  
 85              90              95  
 Ile Ser Ser Val Glu Lys Lys Leu Met Ala Phe Gln Pro Ala Pro Lys  
 100             105             110  
 Val Ile Arg Cys Met Thr Asn Thr Pro Val Val Val Gln Glu Gly Ala  
 115             120             125  
 Thr Val Tyr Ala Thr Gly Thr His Ala Leu Val Glu Asp Gly Gln Leu  
 130             135             140  
 Leu Glu Gln Leu Met Ser Ser Val Gly Phe Cys Thr Glu Val Glu Glu  
 145             150             155             160  
 Asp Leu Ile Asp Ala Val Thr Gly Leu Ser Gly Ser Gly Pro Ala Tyr  
 165             170             175  
 Ala Phe Met Ala Leu Asp Ala Asp Gly Gly Val Lys Met Gly Leu Pro  
 180             185             190  
 Arg Arg Leu Ala Ile Gln Leu Gly Ala Gln Ala Leu Leu Gly Ala Ala  
 195             200             205  
 Lys Met Leu Leu Asp Ser Glu Gln His Pro Cys Gln Leu Lys Asp Asn  
 210             215             220  
 Val Cys Ser Pro Gly Gly Ala Thr Ile His Ala Leu His Phe Leu Glu  
 225             230             235             240  
 Ser Gly Gly Phe Arg Ser Leu Leu Ile Asn Ala Val Glu Ala Ser Cys  
 245             250             255  
 Ile Arg Thr Arg Glu Leu Gln Ser Met Ala Asp Gln Glu Lys Ile Ser  
 260             265             270  
 Pro Ala Ala Leu Lys Thr Leu Leu Asp Arg Val Lys Leu Glu Ser  
 275             280             285  
 Pro Thr Val Ser Thr Leu Thr Pro Ser Ser Pro Gly Lys Leu Leu Thr  
 290             295             300  
 Arg Ser Leu Ala Leu Gly Gly Lys Lys Asp  
 305             310

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2278458

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGCCATCAG CGGCCGGGA GATATCGGCC GGGGGAGAAT AGGGTTGCAC CATCCCAGAA  
 GCTGCTGTTA GCTCGCCGGT CCTCGGCACG CGGCCCGTTC GCCCCCTGCGC TGTCGGCCT

60  
120

TCCCTCTGGCG	TTACTTTCGG	TCCCTCGCTG	AGGGGGTTCG	TCCGGCTCCC	AGGAGGCCTG	180
AACCGCGGAC	CATGAGCGTG	GGCTTCATCG	GGGGCCGCCA	GCTGGCTAT	GCTCTGGCGC	240
GGGGCTTCAC	GGCCGCAGGG	ATCTCTCGG	CTCACAAAGT	ATAAGCCACG	TCCCCAGAAA	300
TGAACTTCCC	TACCGTGTCC	GGCCCTCAGGA	AGATGGGTG	GAACCTGACA	CGCAGCAACCA	360
AGGAGACGGT	GAAGCACAGC	GACGTCTGT	TTCTGCTGT	GAAGCCACAT	ATCATCCCC	420
TCATCCCTGA	TGAGATTGGG	GCGGACGTG	AAGCCAGACA	CATCGTGGTC	TCCCTGTGCGG	480
CTGGTGTACAC	CATCAGCTCT	GTGGAGAAAGA	AGCTGATGCG	ATTCAGGCCA	GCCCCCAAAG	540
TGATTCCTGT	CATGACCAAC	ACACCTGTG	TAGTCAGGAG	AGGGCTCTACA	GTGTACGCCA	600
CGGGCTCTGG	TGCCCCCTGGT	AGGAGATGGG	AGCTCTTGG	CGACGCTCATG	AGCACCGTGG	660
GCTCTCTGAC	TGAGGTGAA	GAGGACCTCA	TCGATGCCGT	CACGGGGCTC	ATGGCCAGGG	720
GGCCCTGCCTA	TGCAATTCTATG	GCTCTGACCG	CATTGGCTGA	TGTTGGGGTG	AAGATGGGT	780
TGCCAACGGCG	CCTGGCAATC	CAACTGGGG	CCCCAGCTT	GCTGGGGAGT	GCCAAGATGC	840
TGCTGGACTC	GGAGCACGAT	CCATGGCCAG	TAAAGGACAA	TCTCTGCTCC	CCTGGGGAGG	900
CCACCATCTAC	TGCTTCTGGAC	TGTTTCTAGAG	GTGGGGGCTT	CCGGCTCTCG	CTCATCAATG	960
CAGTTGAGGC	CTTCTGTATC	CGAACACAGAG	AGCTCACAGTC	CATGGCCGAC	CAAGAAAAAGA	1020
TCTCCCAACG	TGCCCCCTTAAG	AAAGCCCTCT	TAGACAGAGT	GAAGCTGGAA	TCCCCCACAG	1080
TCTCCACACT	GACCCCTCTCC	GACCCAGGAG	AGCTCTTCAC	AAGAAGCCTG	GCCCTGGGAG	1140
GCAAGAAGGA	CTAACGGCAG	ATCTGTCCTC	TCTGTGATTC	AGAGCCCTTA	GTGAGAGCC	1200
CCTCCCCCCC	CTGGCAATCC	CCTGGCCCG	TCCCACCAT	GCCCCCTCCCTC	AGCTGTGCAA	1260
GGAGAAAGCA	TGCTTAGGAA	TGTTTCAGGT	CCTTGTGATA	AAACCTCTT	AAATCTGTT	1320
AGACCAAGCA	ATGGCGACTT	CCCTCTCTGT	CCCATGTTGG	AAAGTTGCTCT	GAAGGGGTGG	1380
TAGATGCTGG	AAGGCGAGCA	ACACCTCTGC	TACGCTGCTC	ATGGTGTGGA	GACTGGGGCT	1440
GGGACTGGAG	TCAGGGCCAG	TGGGAGGGAG	GCTCTGGGAG	GATCTGCAAC	TGAACCCCGA	1500
GGCAGGGTGTG	GTGTGATGCC	AAAGGCAAATG	GTGTGAGGAGA	AAACAGGAAA	CGGGCTTTCT	1560
CTGATTTGGT	AAATGGGAA	GAAGTGAGCA	ACTTAAGATT	GTCACAAATTA	ATCACAAAGTG	1620
TACAGGATTA	GACTGGGTTT	ATATTTAACT	CTTGTCTCAT	AGGTGTACCA	TTTAAAGAGT	1680
GTTATTTAAT	GCTAAGTTA	ACTGCTTTAA	TTAAAGTTAT	TTTTAAATAT	CAAAAAAAA	1740
AA						1742

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GENBANK
- (B) CLONE: 189498

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ser Val Gly Phe Ile Gly Ala Gly Gln Leu Ala Phe Ala Lys Gly
 1           5           10          15
Phe Thr Ala Ala Gly Val Leu Ala Ala His Lys Ile Met Ala Ser Ser
 20          25          30
Pro Asp Met Asp Leu Ala Thr Val Ser Ala Leu Arg Lys Met Gly Val
 35          40          45
Lys Leu Thr Pro His Asn Lys Glu Thr Val Gln His Ser Asp Val Leu
 50          55          60
Phe Leu Ala Val Lys Pro His Ile Ile Pro Phe Ile Leu Asp Glu Ile
 65          70          75          80
Gly Ala Asp Ile Glu Asp Arg His Ile Val Val Ser Cys Ala Ala Gly
 85          90          95
Val Thr Ile Ser Ser Ile Glu Lys Leu Ser Ala Phe Arg Pro Ala
100         105          110
Pro Arg Val Ile Arg Cys Met Thr Asn Thr Pro Val Val Val Arg Glu
115         120          125
Gly Ala Thr Val Tyr Ala Thr Gly Thr His Ala Gln Val Glu Asp Gly
130         135          140

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PF-0532 US

Arg Leu Met Glu Gln Leu Leu Ser Thr Val Gly Phe Cys Thr Glu Val  
145 150 155 160  
Glu Glu Asp Leu Ile Asp Ala Val Thr Gly Leu Ser Gly Ser Gly Pro  
165 170 175  
Ala Tyr Ala Phe Thr Ala Leu Asp Ala Asp Gly Gly Val Lys Met Gly  
180 185 190  
Leu Pro Arg Arg Leu Ala Val Arg Leu Gly Ala Gln Ala Leu Leu Gly  
195 200 205  
Ala Ala Lys Met Leu Leu His Ser Glu Gln His Pro Gly Gln Leu Lys  
210 215 220  
Asp Asn Val Ser Ser Pro Gly Gly Ala Thr Ile His Ala Leu His Val  
225 230 235 240  
Leu Glu Ser Gly Gly Phe Arg Ser Leu Leu Ile Asn Ala Val Glu Ala  
245 250 255  
Ser Cys Ile Arg Thr Arg Glu Leu Gln Ser Met Ala Asp Gln Glu Gln  
260 265 270  
Val Ser Pro Ala Ala Ile Lys Lys Thr Ile Leu Asp Lys Val Lys Leu  
275 280 285  
Asp Ser Pro Ala Gly Thr Ala Leu Ser Pro Ser Gly His Thr Lys Leu  
290 295 300  
Leu Pro Arg Ser Leu Ala Pro Ala Gly Lys Asp  
305 310 315